

## CLAIMS

1. A computer implemented method for analyzing a case-control genetic association study, the method comprising:
  - (a) providing a spreadsheet program running on a computer;
  - (b) programming the spreadsheet software with a statistical power algorithm configured to analyze a case-control genetic association study;
  - (c) inputting to the spreadsheet program values for parameters defining the genetic association study; and
  - (d) determining, using the power algorithm, the study's power to detect a significant difference in distribution of observed allele frequency in cases and controls for the input parameter values.
2. The method of claim 1, wherein the determined power is displayed in the spreadsheet.
3. The method of claim 1, wherein a plurality of values are input for one or more parameters.
4. The method of claim 3, wherein the determined power is displayed in the spreadsheet.
5. The method of claim 4, further comprising displaying the power results obtained by the determination in graphical form.
6. The method of claim 5, wherein the graphical form is a bivariate plot.
7. The method of claim 1, wherein the parameters defining the genetic association study comprise trait value thresholds used to define case and controls; a number of cases; a ratio of controls to cases; and a desired type I error rate.
8. The method of claim 7, wherein the trait value thresholds used to define case and controls comprise a quantitative trait locus (QTL) frequency; broad sense heritability; dominance effect; case and control tail areas; marker frequencies; and a measure of association between marker and QTL sites.

9. A computer implemented method for analyzing a case-control genetic association study, the method comprising:

- (a) providing a spreadsheet program running on a computer;
- (b) programming the spreadsheet software with a statistical power algorithm configured to analyze a case-control genetic association study;
- (c) inputting to the spreadsheet program a subset of values for parameters defining the genetic association study;
- (d) inputting to the spreadsheet program a desired power of the study to detect a significant difference in distribution of observed allele frequency in cases and controls; and
- (e) determining, using the power algorithm, a complete set of values for parameters defining the genetic association study.

10. The method of claim 9, wherein the parameters defining the genetic association study comprise trait value thresholds used to define case and controls; a number of cases; a ratio of controls to cases; and a desired type I error rate.

11. The method of claim 10, wherein the trait value thresholds used to define case and controls comprise a quantitative trait locus (QTL) frequency; broad sense heritability; dominance effect; case and control tail areas; marker frequencies; and a measure of association between marker and QTL sites.

12. The method of claim 9, wherein the input subset of values excludes a number of cases.

13. The method of claim 12, wherein the complete set of values includes a number of cases.

14. The method of claim 9, wherein determining the complete set of values is an iterative refinement process.

15. A computer program product comprising a computer-usable medium having computer-readable program code embodied thereon relating to analyzing a case-control genetic association study, the computer program product comprising

computer-readable program code for effecting the following steps within a computing system:

(a) configuring a spreadsheet program running on a computer with a statistical power algorithm for analysis of a case-control genetic association study;

(b) receiving to the spreadsheet program values for parameters defining the genetic association study; and

(c) determining, using the power algorithm, the study's power to detect a significant difference in distribution of observed allele frequency in cases and controls for the input parameter values.

16. The computer program product of claim 13, wherein the computer-usable medium comprises at least one of a magnetic medium, an optical medium, a hardware device specially configured to store and perform program instructions, and a carrier wave.

17. The computer program product of claim 13, wherein the parameters defining the genetic association study comprise trait value thresholds used to define case and controls; a number of cases; a ratio of controls to cases; and a desired type I error rate.

18. The computer program product of claim 17, wherein the trait value thresholds used to define case and controls comprise a quantitative trait locus (QTL) frequency; broad sense heritability; dominance effect; case and control tail areas; marker frequencies; and a measure of association between marker and QTL sites.

19. A computer program product comprising a computer-usable medium having computer-readable program code embodied thereon relating to analyzing a case-control genetic association study, the computer program product comprising computer-readable program code for effecting the following steps within a computing system:

(a) configuring a spreadsheet program running on a computer with a statistical power algorithm for analysis of a genetic association study;

(b) receiving to the spreadsheet program a subset of values for parameters defining the case-control genetic association study;

(c) receiving to the spreadsheet program a desired power of the study to detect a significant difference in distribution of observed allele frequency in cases and controls; and

(d) determining, using the power algorithm, a complete set of values for parameters defining the genetic association study.

20. The computer program product of claim 19, wherein the computer-usable medium comprises at least one of a magnetic medium, an optical medium, a hardware device specially configured to store and perform program instructions, and a carrier wave.

21. The computer program product of claim 20, wherein the parameters defining the genetic association study comprise trait value thresholds used to define case and controls; a number of cases; a ratio of controls to cases; and a desired type I error rate.

22. The computer program product of claim 21, wherein the trait value thresholds used to define case and controls comprise a quantitative trait locus (QTL) frequency; broad sense heritability; dominance effect; case and control tail areas; marker frequencies; and a measure of association between marker and QTL sites.

23. A computer system for analyzing a case-control genetic association study, the computer system, comprising:

(a) a computer;

(b) a spreadsheet program running on the computer with a statistical power algorithm for analysis of a case-control genetic association study, the spreadsheet program configured to,

(i) receive program values for parameters defining the genetic association study, and

(ii) determine, using the power algorithm, the study's power to detect a significant difference in distribution of observed allele frequency in cases and controls for the input parameter values.

24. The system of claim 23, wherein the parameters defining the genetic association study comprise trait value thresholds used to define case and controls; a number of cases; a ratio of controls to cases; and a desired type I error rate.

25. The system of claim 24, wherein the trait value thresholds used to define case and controls comprise a quantitative trait locus (QTL) frequency; broad sense heritability; dominance effect; case and control tail areas; marker frequencies; and a measure of association between marker and QTL sites.

26. A computer system for analyzing a case-control genetic association study, the computer system, comprising:

(a) a computer;

(b) a spreadsheet program running on the computer with a statistical power algorithm for analysis of a case-control genetic association study, the spreadsheet program configured to,

(i) receive a subset of values for parameters defining the genetic association study;

(ii) receive a desired power of the study to detect a significant difference in distribution of observed allele frequency in cases and controls; and

(iii) iteratively determine, using the power algorithm, a complete set of values for parameters defining the genetic association study having the desired power.

27. The system of claim 26, wherein the parameters defining the genetic association study comprise trait value thresholds used to define case and controls; a number of cases; a ratio of controls to cases; and a desired type I error rate.

28. The system of claim 27, wherein the trait value thresholds used to define case and controls comprise a quantitative trait locus (QTL) frequency; broad

sense heritability; dominance effect; case and control tail areas; marker frequencies;  
and a measure of association between marker and QTL sites.